



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 125117

TO: Karen A Lacourriere
Location:
Art Unit: 1635
July 26, 2004

Case Serial Number: 09/301380

From: P. Sheppard
Location: Remsen Building
Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

18 d/2

Sheppard, Paula

From: Lacourciere, Karen
Sent: Wednesday, July 21, 2004 3:48 PM
To: Sheppard, Paula
Subject: RE: Sequence search

Hi Paula-
The numbers are
ABA70229
AAI50358
AAK44359
AAK18454
ABS44016
ABS18595
ABA71469
AAI51738
AAK45811

The serial number is 09/301,380 and the sequence these oligos bind to is SEQ ID NO:1
I can bring the original search down to you if it helps. Let me know what you need! Thanks so much, I really appreciate your help.
Karen

-----Original Message-----

From: Sheppard, Paula
Sent: Tuesday, July 20, 2004 5:28 PM
To: Lacourciere, Karen
Subject: RE: Sequence search

Yes. If you can provide the accession numbers of interest and the seq ID used to search it, then I can provide you with alignments and references.

Paula
(571) 272-2529

-----Original Message-----

From: Lacourciere, Karen
Sent: Tuesday, July 20, 2004 2:53 PM
To: Sheppard, Paula
Subject: Sequence search

Hi Paula-
You did a sequence search for me back in May on SN 301,380. Some of the hits which appear in the summary now appear to be potentially useful references, but they are too far down on the list and the detailed summaries were not provided. Is it possible to get more information on these sequences based on the accession numbers?
Thanks-
Karen

Karen A. Lacourciere Ph.D.
Remsen 2D15 GAU 1635
(571) 272-0759

> O <
 O | O IntelliGenetics
 > O <

FastDB ~ Fast Pairwise Comparison of Sequences
 Release 5.4

Results file 1_x_listing_inv.res made by spaula on Mon 26 Jul 104 14:24:17-PDT.

Query sequence being compared:US-09-301-380-1' (1-4134)
 8
 Number of sequences searched:
 8
 Number of scores above cutoff:

Results of the initial comparison of US-09-301-380-1' (1-4134) with:

File : aa150358.seq
 File : aa151738.seq
 File : aak18454.seq
 File : aak44359.seq
 File : aak5811.seq
 File : abaa1469.seq
 File : abs18595.seq
 File : abs44016.seq

100-

U

M

B

E

R

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C

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SEARCH STATISTICS		PARAMETERS		SEARCH STATISTICS		PARAMETERS		SEARCH STATISTICS		PARAMETERS	
Scores:	Mean	Median	Standard Deviation	Similarity matrix	Unitary	K-tuple	Joining penalty	Similarity matrix	Unitary	K-tuple	Joining penalty
Times:	00:00:00.90	00:00:00.00	Total Elapsed	Mismatch penalty	1	4	30	Mismatch penalty	1	4	30
Number of residues:	2676	2676	PT	Gap penalty	1.00	Window size	500	Gap penalty	1.00	Window size	500
Number of sequences searched:	8	8	PS	Gap size penalty	0.33	0	0	Gap size penalty	0.33	0	0
Number of scores above cutoff:	8	8	XX	Cutoff score	0	0	0	Cutoff score	0	0	0
Randomization group	0	0	XX	Randomization group	0	0	0	Randomization group	0	0	0
Score:	182	225	84.92	Score:	182	225	84.92	Score:	182	225	84.92
Times:	00:00:00.90	00:00:00.00	Total Elapsed	Times:	00:00:00.90	00:00:00.00	Total Elapsed	Times:	00:00:00.90	00:00:00.00	Total Elapsed
Number of residues:	2676	2676	PT	Number of residues:	2676	2676	PT	Number of residues:	2676	2676	PT
Number of sequences searched:	8	8	PS	Number of sequences searched:	8	8	PS	Number of sequences searched:	8	8	PS
Number of scores above cutoff:	8	8	XX	Number of scores above cutoff:	8	8	XX	Number of scores above cutoff:	8	8	XX
The scores below are sorted by initial score.				The scores below are sorted by initial score.				The scores below are sorted by initial score.			
Significance is calculated based on initial score.				Significance is calculated based on initial score.				Significance is calculated based on initial score.			
A 100% identical sequence to the query sequence was not found.				A 100% identical sequence to the query sequence was not found.				A 100% identical sequence to the query sequence was not found.			
The list of best scores is:				The list of best scores is:				The list of best scores is:			
Sequence Name	Description	Length	Score	Sequence Name	Description	Length	Score	Sequence Name	Description	Length	Score
1. aak18454	Human brain expressed single	230	230	1. aak18454	Human brain expressed single	230	230	1. aak18454	Human brain expressed single	230	230
2. aak14359	Human bone marrow expressed s	230	230	2. aak14359	Human bone marrow expressed s	230	230	2. aak14359	Human bone marrow expressed s	230	230
3. abs18595	Human genome-derived single e	230	230	3. abs18595	Human genome-derived single e	230	230	3. abs18595	Human genome-derived single e	230	230
4. abs44016	Human liver single exon probe	230	230	4. abs44016	Human liver single exon probe	230	230	4. abs44016	Human liver single exon probe	230	230
5. aak15811	Human foetal liver single exo	224	224	5. aak15811	Human foetal liver single exo	224	224	5. aak15811	Human foetal liver single exo	224	224
6. aba17469	* *** 1 standard deviation below mean	224	224	6. aba17469	* *** 1 standard deviation below mean	224	224	6. aba17469	* *** 1 standard deviation below mean	224	224
7. aai150358	TOIG of: aai150358 check: 446	611	289	7. aai150358	TOIG of: aai150358 check: 446	611	289	7. aai150358	TOIG of: aai150358 check: 446	611	289
8. aa151738	TOIG of: aa151738 check: 878	697	35	8. aa151738	TOIG of: aa151738 check: 878	697	35	8. aa151738	TOIG of: aa151738 check: 878	697	35
1. US-09-301-380-1' (1-4134)	Human brain expressed single exon probe SEQ ID NO: 10417454	10417454	10417454	1. US-09-301-380-1' (1-4134)	Human brain expressed single exon probe SEQ ID NO: 10417454	10417454	10417454	1. US-09-301-380-1' (1-4134)	Human brain expressed single exon probe SEQ ID NO: 10417454	10417454	10417454
TOIG of: aak18454	check: 7397 from: 1 to: 230			TOIG of: aak18454	check: 7397 from: 1 to: 230			TOIG of: aak18454	check: 7397 from: 1 to: 230		
ID	AAK18454 standard; DNA; 230 BP.	XX		ID	AAK18454 standard; DNA; 230 BP.	XX		ID	AAK18454 standard; DNA; 230 BP.	XX	
AC	AAK18454;	XX		AC	AAK18454;	XX		AC	AAK18454;	XX	
DT	05-NOV-2001 (first entry)	XX		DT	05-NOV-2001 (first entry)	XX		DT	05-NOV-2001 (first entry)	XX	
DB	Human brain expressed single exon probe SEQ ID NO: 104455.	XX		DB	Human brain expressed single exon probe SEQ ID NO: 104455.	XX		DB	Human brain expressed single exon probe SEQ ID NO: 104455.	XX	
KW	Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer; ss.	XX		KW	Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer; ss.	XX		KW	Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer; ss.	XX	
KW	Homo sapiens.	XX		KW	Homo sapiens.	XX		KW	Homo sapiens.	XX	
OS		XX		OS		XX		OS		XX	
PN		XX		PN		XX		PN		XX	
XX		XX		XX		XX		XX		XX	
PD		XX		PD		XX		PD		XX	
09-AUG-2001.		XX		09-AUG-2001.		XX		09-AUG-2001.		XX	
XX		XX		XX		XX		XX		XX	
PR		XX		PR		XX		PR		XX	
30-JAN-2001; 2001W0-US000667.		XX		30-JAN-2001; 2001W0-US000667.		XX		30-JAN-2001; 2001W0-US000667.		XX	
PR		XX		PR		XX		PR		XX	
04-FEB-2000; 2000US-0180312P.		XX		04-FEB-2000; 2000US-0180312P.		XX		04-FEB-2000; 2000US-0180312P.		XX	
26-MAY-2000; 2000US-0201456P.		XX		26-MAY-2000; 2000US-0201456P.		XX		26-MAY-2000; 2000US-0201456P.		XX	
30-JUN-2000; 2000US-0060840B.		XX		30-JUN-2000; 2000US-0060840B.		XX		30-JUN-2000; 2000US-0060840B.		XX	
03-AUG-2000; 2000US-00632366.		XX		03-AUG-2000; 2000US-00632366.		XX		03-AUG-2000; 2000US-00632366.		XX	
21-SEP-2000; 2000US-0234687P.		XX		21-SEP-2000; 2000US-0234687P.		XX		21-SEP-2000; 2000US-0234687P.		XX	
27-SEP-2000; 2000US-0236359P.		XX		27-SEP-2000; 2000US-0236359P.		XX		27-SEP-2000; 2000US-0236359P.		XX	
04-OCT-2000; 2000GB-00024263.		XX		04-OCT-2000; 2000GB-00024263.		XX		04-OCT-2000; 2000GB-00024263.		XX	
PA		XX		PA		XX		PA		XX	
(MOLE-) MOLECULAR DYNAMICS INC.		XX		(MOLE-) MOLECULAR DYNAMICS INC.		XX		(MOLE-) MOLECULAR DYNAMICS INC.		XX	
PI		XX		PI		XX		PI		XX	
Perrin SG, Hanzel DK, Chen W, Rank DR;		XX		Perrin SG, Hanzel DK, Chen W, Rank DR;		XX		Perrin SG, Hanzel DK, Chen W, Rank DR;		XX	
WPI; 2001-483446/52.		XX		WPI; 2001-483446/52.		XX		WPI; 2001-483446/52.		XX	
Single exon nucleic acid probes for analyzing gene expression in human brains.		XX		Single exon nucleic acid probes for analyzing gene expression in human brains.		XX		Single exon nucleic acid probes for analyzing gene expression in human brains.		XX	
Example 4; SEQ ID NO 104455; 650pp + Sequence Listing; English.		XX		Example 4; SEQ ID NO 104455; 650pp + Sequence Listing; English.		XX		Example 4; SEQ ID NO 104455; 650pp + Sequence Listing; English.		XX	
The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention		CC		The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention		CC		The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention		CC	
XX		CC		XX		CC		XX		CC	

SQ Sequence 230 BP; 45 A; 61 C; 44 G; 80 T; 0 U; 0 Other;
 AAK4354 Length: 230 July 26, 2004 14:10 Type: N Check: 7397 ..

Initial Score = 230 Optimized Score = 230 Significance = 0.57
 Residue Identity = 100% Matches = 230 Mismatches = 0
 Gaps = 0

90 100 110 X 120 130
 AACATTCAGAGAAATGGGATAATGGCTTGGCTTGACAGG
 AGGATTATGGCSTTGAAGG
 X 10 20

140 150 160 170 180 190 200
 AGAAGGTGCCCTGAGCTTCTGGCTTCCCTAGCCGGCTTTCTGCCTTCTACACTGTATGGCCAATAAA
 AGAAGGTGCCCTGAGCTTCTGGCTTCTGGCTTCCCTAGCCGGCTTTCTGCCTTCTACACTGTATGGCCAATAAA
 30 40 50 60 70 80 90

210 220 230 240 250 260 270
 GAGGCCATCTCATGAACTGCGGATAAACCCCTCTCATAGTCACACTGGCTGTGATCTCTTCT
 GGRGCCATCTCATGAACTGCGGATAAACCCCTCTCATAGTCACACTGGCTGTGATCTCTTCT
 100 110 120 130 140 150 160

280 290 300 310 320 330 340 X 350
 TTTCACAGTCGCTGCTGAAGGAGTGCAGTCCTCCCTTTCAAGGCTTGTGCTCTGTGATCTGTGATT
 TTTCACAGTCGCTGCTGAAGGAGTGCAGTCCTCCCTTTCAAGGCTTGTGCTCTGTGATCA
 170 180 190 200 210 220 230

360 370 380 390
 TCCAAATGTCATCATCTCTCATAGGTGATTTCAGG

2. US-09-301-380-1' (1-4134)
 Human bone marrow expressed single exon probe SEQ ID NO: 18916.
 aak4359 Human bone marrow expressed single exon probe SEQ ID NO: 18916.

TOIG of: aak4359 check: 7397 from: 1 to: 230
 ID AAK4359 standard; DNA; 230 BP.
 XX AAK4359;
 AC 06-NOV-2001 (first entry)
 DE Human bone marrow expressed single exon probe SEQ ID NO: 18916.
 KW Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
 XX Homo sapiens.
 OS WO200157276-A2.
 PN 09-AUG-2001.
 PD XX
 PF 30-JAN-2001; 2001WO-US0006668.
 PR 04-FEB-2000; 2000US-0180312P.
 PR 06-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-0207456P.
 PR 03-AUG-2000; 2000US-00632366.
 PR 27-SEP-2000; 2000US-0214687P.
 PR 04-OCT-2000; 2000GB-00024263.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR ; 2001-488900/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.
 XX Example 4; SEQ ID NO 18916; 658BP + Sequence Listing; English.

CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukemia and myeloma. The present sequence is one of
 CC the probes of the invention
 XX Sequence 230 BP; 45 A; 61 C; 44 G; 80 T; 0 U; 0 Other;
 SQ Sequence 230 BP; 45 A; 61 C; 44 G; 80 T; 0 U; 0 Other;
 AAK4359 Length: 230 July 26, 2004 14:10 Type: N Check: 7397 ..
 Initial Score = 230 Optimized Score = 230 Significance = 0.57
 Residue Identity = 100% Matches = 230 Mismatches = 0
 Gaps = 0

70 80 90 100 110 X 120 130
 AACATTCAGAGAAATGGGATAATGGCTTGGCTTGACAGG
 AGGATTATGGCSTTGAAGG
 X 10 20

140 150 160 170 180 190 200
 AGAAGGTGCCCTGAGCTTCTGGCTTCCCTAGCCGGCTTTCTGCCTTCTACACTGTATGGCCAATAAA
 AGAAGGTGCCCTGAGCTTCTGGCTTCCCTAGCCGGCTTTCTGCCTTCTACACTGTATGGCCAATAAA
 30 40 50 60 70 80 90

210 220 230 240 250 260 270
 GAGGCCATCTCATGAACTGCGGATAAACCCCTCTCATAGTCACACTGGCTGTGATCTCTTCT
 GGRGCCATCTCATGAACTGCGGATAAACCCCTCTCATAGTCACACTGGCTGTGATCTCTTCT
 100 110 120 130 140 150 160

280 290 300 310 320 330 340 X 350
 TTTCACAGTCGCTGCTGAAGGAGTGCAGTCCTCCCTTTCAAGGCTTGTGCTCTGTGATCTGTGATT
 TTTCACAGTCGCTGCTGAAGGAGTGCAGTCCTCCCTTTCAAGGCTTGTGCTCTGTGATCA
 170 180 190 200 210 220 230

360 370 380 390
 TCCAAATGTCATCATCTCTCATAGGTGATTTCAGG

3. US-09-301-380-1' (1-4134)
 abs1895 Human genome-derived single exon probe ORF from lung SEQ ID NO 18586.
 TOIG of: abs1895 check: 7397 from: 1 to: 230
 ID ABS1895 standard; DNA; 230 BP.
 XX ABS1895;
 AC ABS1895;
 XX DT 19-AUG-2002 (first entry)
 XX DE Human genome-derived single exon probe ORF from lung SEQ ID NO 18586.
 XX KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary hamosiderosis;
 KW pulmonary histiocytosis; lymphangiomyomatosis; Kartagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocytic pulmonary dysplasia;
 KW primary ciliary dyskinesis; pulmonary hypertension;
 KW hyaline membrane disease; open reading frame; ORF.
 XX OS Homo sapiens.

XX WO200186003-A2.
 PN XX
 PD 15-NOV-2001.
 PF 30-JAN-2001; 2001WO-US000665.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632666.
 PR 21-SEP-2000; 2000US-0234887P.
 PR 27-SEP-2000; 2000US-0236393P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR; 2002-114183/15.
 XX PT spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.
 PS XX
 Claim 4; SEQ ID NO 18586; 634pp; English.
 XX The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes ; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarray having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene, a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemoiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, Kartagener syndrome, fibrocytic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe open reading frame of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)
 SQ Sequence 230 BP; 45 A; 44 G; 80 T; 0 U; 0 Other;
 ABS18595 Length: 230 July 26, 2004 14:11 Type: N Check: 7397 ..
 Initial Score = 230 Optimized Score = 230 Significance = 0.57
 Residue Identity = 100% Matches = 230 Mismatches = 0
 Gaps = 0 Conservative Substitutions = 0
 XX
 XX DR; 2001-488898/53.
 XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human adult liver.
 XX
 Claim 4; SEQ ID NO 19006; 658pp; English.
 XX
 CC The invention relates to a single exon nucleic acid probe (SENPD) (I)
 WPL: 2001-488898/53.

B. US-09-301-380-1' (1-4134)
aa11738 TOIG of: aa151738 check: 8787 from: 1 to: 697
TOIG of: aa151738 check: 8787 from: 1 to: 697
LOCUS AA151738 697 bp mRNA linear EST 14-MAY-1997
DEFINITION z12h03 Soares-pregnant uterus NbHPV Homo sapiens cDNA clone IMAGE:503285 5' similar to contains element MER22 repetitive element ; mRNA sequence.
AA151738
ACCESSION AA151738.1 GI:1720293
VERSION AA151738.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Butelostomii; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 697)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., Dubuge,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucca,B., Lacy,M., Le,N., Mardis,E., Moore,S., Morris,M., Parsons,J., Prange,C., Riekin,L., Rohlfing,T., Scheibenbogen,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Tsvaykis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R., and Marra,M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
PUBMED 9704478
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LiNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Insert length: 813 Std Error: 0.00
Seq. Primer: -28M13 rev2 from Amersham
High Quality Sequence stop: 513.
Location/Qualifiers
1. 697
/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="GDB:3808273"
/db_xref="Taxon:9566"
/clone="IMAGE:503285"
/sex="female"
/dev_stage="adult"
/lab_hoss="DHLOB"
/clone_lab="Soares pregnant uterus NbHPV"
/note="Organ: uterus; Vector: PT73-Pac; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
O190 (dtr) primer (5'-AACGGAAAGATCGGGCGCCCTTTTTTTTTTTT 3'),
double-stranded cDNA was digested to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified PT73 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."
ORIGIN AA151738 Length: 697 July 26, 2004 14:11 Type: N Check: 8787 ..
Initial Score = 35 Optimized Score = 287 Significance = -1.73
Residue Identity = 45% Matches = 376 Mismatches = 305
Gaps = 148 Conservative Substitutions = 0
AA151738
CAGTTTCCAGGAGCCACCATGGAGGTCTCCGAATACTACA-GCT-GGCTGGGGCA
X 10
3640 3580 3550 3460 3410 3420
AGTTTCTTGTCGACTGAAACTCTCACTGTTGAAANGAATTATCCAAATATTATA
-GT--AAATAACCTAGGCATGTCCTAGGG-AGAAGTTAA---TGACC-----
430 440 450 460 470
3570 3550 3520 3530 3540 3550 3560
CCTGGTGTAACTCAATGGGGCTCGAGGAAGTACTAAGACTGTTGATGTTCA
-GT--TGCTTGTCTTGTAA-AATGTTGTCGNGATGTCCTGA-----ANTGGTTAA
530 540 550 560 570
3640 3660 3670 X 3680 3690 3700
AG-ACCTTG---GCANGGAGAAATAAGTTAAAG
530 540 550 560 570
3710 3720
AGCGTTCTGTGCC

1540 1550 1560 1570 1580 1590 1600
 AACCCCATGTCATCAGGGCTGAACTTGTGATCGGTATG-GAACAAAGTTGGCTGACATATA
 ATTCAAAAGT-TCCAGAGNN
 20 30 40 50 60 70 80
 1610 1620 1630 1640 1650 1660 1670
 TTGGATAACATTGCCAACACCAGATGTTCCATTATCACCATCTTCTGGCCAGCTAACATTGTA
 NNNG-NNNAT--CC-----CNGAANTAGATTCT-----TCCTGTT-----CTAAGATTCTA
 90 100 110 120 130
 1680 1690 1700 1710 1720 1730 1740
 CGAAGGGCTGGCCATTAGATTGAAACCATAAGGCTTCCAGTAATCICCAAATTATAAGGCTCTGA
 -GATCAGATGTCACCAAGATTGATGTTAA-----TA-----AGATTCTAACGGCTCTGT
 140 150 160 170 180
 1750 1760 1770 1780 1790 1800 1810 1820
 TCCAGAGCTTCCACAGTGTGGGTTTATCTGGTTGAGCTTCTGGCTAACATACTGCTCAGACGGCTC
 T---CTGT-TT-CAGGGACTCTAGTGTAA-----TA-----AGATCTCGG---GATCCT-----AAGNATC
 190 200 210 220 230
 1830 1840 1850 1860 1870 1880
 GCTGGG-GAAGCTC---TTCCCAATGCGTCACTGCCATCACSGGGAGAGGAGTAGTCTCACTGAA
 NAAGGGANAGAGGCACACNCAGNNAGGGNNAGAGANCAAAAGGNAATA-ANGTCNAANGNTGGACACC
 240 250 260 270 280 290 300
 1890 1900 1910 1920 1930 1940 1950
 GCTTCAG-CTGGCTCTGGCTCTGTGTCAGTCACTGCACTGTTGGCTGCCAACGGCTGCTGCGAT
 NNTAGGGCTTGTGCAATTGCTAGCTAGACCAT-GGTAAAGTCTAAAGGATTCAGAACATTCTAA-
 310 320 330 340 350 360 370
 1960 1970 1980 1990 2000 2010 2020
 TGCATCTATA-TTCGATG---ATGAATTGTAATGGCTATGGCTATTGTTGTCATGCCCTGGCTCATGACAG
 --ATCTT-ATAGTTCTAGGACTGTA-GTCTAA-GACTAAATGTTCTAAAGGATTCAGAACATTCTAA-
 380 390 400 410 420 430 440
 2030 2040 2050 2060 2070 2080 2090 2100
 CTGAAACACTTGTCAACTTGATCTGTCACTGTTCTAACTGAAAGGGAGGATTTGGACATCGTAAACGGAGC
 GTCACA---GTTCTAG---ACTATAGTGTGCAATTCAAGG-----TTCTAAC---CTTAACTCTGAT
 450 460 470 480 490
 2110 2120 2130 2140 2150 2160 2170
 TGAGGTGGAGTAGGCAACACGCTGAACTGCTGATCGTCACTGACATCACTAACATAGT-GTCCAGTGGCTGTC
 ATTCCTGGGT-GCCCTCTCTCTAG-TATC-ATTGTCCTC-CTCCTCACTG---TGTG---TGTG---
 500 510 520 530 540 550
 2180 2190 2200 2210 2220 2230 2240
 ACACGTGAGGCTCCGCTGATCGTCACTGACATCACTAACATAGT-GTCCCTGTCACAG-TGAA
 ---GGGT---GTCCTCTCTAG-TGCTGGCTGCAAT-GC-ATTA-GGGATGCTCCCTTCGGAGATGGA
 560 570 580 590 600 610
 2250 2260 2270 2280 2290 2300 2310
 CCTTTCATCATCGGCACTTCCGTTCTGTCAGCCA-CAGGACACTGAGGGATAAGGTGTGATCATGTT
 CGATTCTACCTTTC-EGGCTCATG-TGCTGGCTGACATCCCACCTCTGAGA-NAGATGTGATC-TGTC
 620 630 640 650 660 670 680
 2320 2330 2340 2350 2360 2370
 TCACCTTCATTCAAAGGACACCTGCTCCCTTGTGACAACTGCAATTGCGCTTAAGTGA
 TCAAGGGGNAGTCAC
 690 X

AACTGGAGAATTCGCGCCCTTTTTTTTTT 3',
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pRm3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

ORIGIN

A1150358 Length: 611 July 26, 2004 14:10 Type: N Check: 4462 ..

Initial Score = 497	Optimized Score = 280	Significance = 0.98	1410	1420	1430	1440	1450	X
Residue Identity = 130	Matches = 363	Mismatches = 237	TATCGGAATGCTCAATGATAATTACTGGCA--AACGCATTGTAATGCTGCTAGC					X
Gaps =	Conservative Substitutions = 0		TGTC-CTGAATTGACATAAGGAA--ATAAGTTAAG					

700 710 720 730 740 750 760
AGAGTTCTCAAGGGACCTTGATGGGACCTTATTTCATGCTCCAGAGGACACCCTGAT
X AAGAAC-CAGGTTAG--AT

770 780 790 800 810 820 830
ATCGTATGCTAGATTAATCATCTAACATACAGAGGAACTTATCTGTGAAAGTGATTCA
TCTTITTAAG-TACA-TTGTGTT---GATGTTCCACAGAAC-ACCT-T-----AAG-TGTTACT
20 30 40 50 60 70

840 850 860 870 880 890 900
GTCGATGATGATGATGACACTATAGTCGTAAT-TTG-AGTGACACTGAGTTTATGGCTAAATCAGTA
GTTG-TG---TAATGTCCTCTGAAAGG -AACCTGTCTAAACCTGGTT-TGCTGTTTGGAGTT
80 90 100 110 120 130

910 920 930 940 950 960 970
GAGAGGOCACCACTTTAACTCCAGAAGSCA-ATGCAAGTAAGAGGAAATTAGGGAATGTC
TCFA---CCTAAATCATTTT-----GGTATATCCTGATAATCTCTA-TAA-TACTA-GAATTG
140 150 160 170 180 190

980 990 1000 1010 1020 1030 1040
CTTCACTGGAGTGCATGAGAGGACTGCCAACCAAATTATTACTGGCAAAGGAGATGGCA
CT-GCA---AAATATGT-AAGAGAATG--GAGGCTTAAT-----AGCT-GATTCCT-
200 210 220 230

1050 1060 1070 1080 1090 1100 1110
CCCCAAAACAGGACAGTTATAAGAACTTGGAAACCTGGAGATCATGGTTGAGGAGACTCT
CCCA-ATTTA-TCTG-TTAT---GTTTGTACTA--TT-CACAT-TTATGCTTT---TC-TACGAT
250 260 270 280 290

1120 1130 1140 1150 1160 1170 1180
GGAAATTAACCAATGTA-TAGCAAAAATGATAGGACCATCACCATACTTGTGAGTTAACGC
AAAATGTTGATTTGATGCCA-GTA-TAGGAACCICAATC-TTGTGTTTGTGCTTAAAGA
300 310 320 330 340 350

1200 1210 1220 1230 1240 1250 1260
GGCTCCATACTGGATCACGGCCCTCAAATCTGGTGTG-CTGCCCCAGAGGAGTGGACCTTGATC-TGC
AGGTTTCAGT-TGTTA---CCTCAAGGTATTCTGAGTGT CCTATTGCTTAATAGGAAATACTTCC
360 370 380 390 400 410 420

1270 1280 1290 1300 1310 1320
AGAGCT---ATGGCAACCCAAACCGAAATTAGCTGGTAAACAATGGACCTCCAAATGTTAAGGAGACT
CAAGCTGAAATTAAAGTTC--TCCPA-AATTGAGATCCAAATCTATGTAATA-ACCTAG-GCAT
430 440 450 460 470 480 490

1330 1340 1350 1360 1370 1380 1390
GATGCAAGGAAATAATGAGGATACCATTTTCAATGTTAAGGAGATAAGTGGAGTA
GA-GTCCCCTAG-GGAGAGTAAAGTGCCTAATGAGA-NTGGTTAAAGTGCCTAATGAGGAGCTATGAG
500 510 520 530 540 550

1480 1490 1500
CACCAAGATCCCTCACACTGCAAACACACTCTACAG

2. US-09-301-380-1 (1-4134)
aaK18454 Human brain expressed single exon probe SEQ ID NO:

TOIG of: aaK18454 check: 7397 from: 1 to: 230
ID AAk18454 standard; DNA; 230 BP.
XX AC AC
AAK18454;
XX

DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe SEQ ID NO: 18445.
XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;
Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
KW ss.
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PR 09-AUG-2001.
XX PF 30-JAN-2001; 2001W0-US000667.
XX PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-0063408.
PR 03-AUG-2000; 2000US-00633366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-02236339P.
PR 04-OCT-2000; 2000US-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PS WPI; 2001-483446/52.

XX PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX DR
XX XX

XX PS Example 4 ; SEQ ID NO 18445; 650pp + Sequence Listing; English.
XX XX

XX CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX SQ Sequence 230 BP; 45 A; 61 C; 44 G; 80 T; 0 U; 0 Other;
XX XX

AAK18454 Length: 230 July 26, 2004 14:10 Type: N Check: 7397 ..

Initial Score = 71	Optimized Score = 111	Significance = 0.68
Residue Identity = 52%	Matches = 139	Mismatches = 84
Gaps = 42	Conservative Substitutions = 0	

420 430 440 450 460 470 480
GGAACGGTCATTTAACATCATGAGGAAGGGAAAGCTGAGACCTATGAGGAGCTATGAG

US-09-301-380-1 (1-4134)
aak44359 Human bone marrow expressed single exon probe SEO
TGCTA

TOIG of: aak4359 check: 7397 from: 1 to: 230
D AAK4359 standard; DNA; 230 BP.
X
C AAK4359;
X
T 06-NOV-2001 (first entry)
X Human bone marrow expressed single exon probe SEQ ID NO: 18916.
X microarray; cancer; leukaemia; lymphoma; myeloma; ss.
X

sapiens.

TGCTA

110

1118-08-301-380 1 (1 1774)

DR WPI; 2001-488908/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing PT gene expression in human adult liver.

XX Claim 4, SEQ ID NO 19006; 658pp; English.

CC The invention relates to a single exon nucleic acid probe (SENPs) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements / fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver.

CC (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinemia, hyperlipidaemia and hypercholesterolemia which is associated with coronary heart disease. AB25011-AB551005 represent human liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 230 BP; 45 A; 61 C; 44 G; 80 T; 0 U; 0 Other;

SQ ABS4406 Length: 230 July 26, 2004 14:11 Type: N Check: 7397 ..

Initial Score = 71	Optimized Score = 111	Significance = 0.68
Residue Identity = 52%	Matches = 139	Mismatches = 84
Gaps = 42	Conservative Substitutions = 0	

420 430 440 450 460 470 480

GGAAACGGCTCATATAATTAAACATGAGCGAAGGGAAAGCTAGACCTATGGAGGACTTCAAGCTAGGC
AGGAATTCTAGGGCTGTGACGG
X 10 20

490 500 510 520 530 540 550

AAGGAACG-AACGCCGGAGCTGCAAGTTCTATAACATTGGTGTCCGCCATCCAGATCAC-CATTGTGCA
-A-GAAGGTGCCTCTGAGCTTCGTTCTGGCTCT-CTTCAGCCGGCTCT-TTCTCTTCTTACCATGATGT--C
30 40 50 60 70 80

560 570 580 590 600 610 620

CAANGAAAATGTTGACCAATCACACTCAAAAGTGGTAGTCAAGCTTGTAGTCACTCCCTGCAAGAACCCCCAAATGG
-C-AATAAAG---GAGCC-ATC-CTCATTTGAACTGGCA--TAAACCCCT--CTCCATA-GTCRACATAG
90 100 110 120 130 140

630 640 650 660 670 680 690

ATTACCAACCTATAATTTGATGGATAATTCTTC- AAAGACTTCCAAGAGTGAGAGTTCT
GCTGNGTCA-CTATCTCTTT--TTCGA-CAGTCCTGCTGAGGGAGTGCATTCT
150 160 170 180 190 200

700 710 720 X 730 740 750 760 770

C-AAGGTTGATGGGACCTTATTTCCTCAATGTCCTCCAGGGACACCCGGAAAGACTATCTGTA
-CAAGGCTTG--TGTCTCTGTCATCA
210 220 230

TGCTA

2600 2610 2620 2630 2640 2650

GGGGTTGCG --CCCGAGGCGGCCATAGCTGATGG-GACATTCTGAGAAAGACTTCCAAATGGCTCTGG
AATATA-TTCTCTCAAGGCAAGCCATCCATGCTGAGCTGCTGAGCTGCTGAGCTGCTGAGCTG
90 100 110 120 130

2670 2680 2690 2700 2710 2720

GAAACGGCCCTGATGTCGTTGAAAG-TACCTTAG- CGGAGGTCACATGGGACCCAGTACCTCTGAGAG
-AAGGTTGCGCTGAGCA-ATATATT-TGGTACATTGCAAAC- CACAGATG-TCCATT
150 160 170 180 190 200

6. US-09-301-380-1 (1-4134)

aak45811 standard; DNA; 224 BP.

XX Human bone marrow expressed single exon probe SEQ XX

TOIG of: aak45811 check: 7602 From: 1 to: 224

XX aak45811 standard; DNA; 224 BP.

AC AAK45811;

2740 X 2750 2760 2770 2780 2790
 CATTCAAGGG
 220 X

7. US-09-301-380-1 (1-4134)
 ab71469 Human foetal liver single exon nucleic acid probe
 TOIG of: ab71469 check: 7602 from: 1 to: 224
 ID ABA71469 standard; DNA; 224 BP.
 XX
 AC ABA71469;
 XX DT 01-FEB-2002 (first entry)
 XX DE Human foetal liver single exon nucleic acid probe #19774.
 XX KW Human; Foetal liver; gene expression; single exon nucleic acid probe; ss.
 XX OS Homo sapiens.
 XX PN WO20015277-A2.
 XX PD 09-AUG-2001.
 XX PP 30-JAN-2001; 2001WO-US000669.
 XX PR 04-FEB-2000; 2000US-0160312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00532366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-02326359P.
 XX PR 04-OCT-2000; 2000USB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-4-83447/5Z.
 XX PT SEQ ID NO 19774; 63pp + Sequence Listing; English.
 XX CC The invention relates to a single exon nucleic acid probe for analyzing
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human fetal liver. The
 CC present sequence is a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at [ftp://ftpi.wipo.int/pub/published_pct_sequences](http://ftpi.wipo.int/pub/published_pct_sequences)
 XX SQ Sequence 224 BP; 58 A; 59 C; 49 G; 58 T; 0 U; 0 Other;
 ABA71469 Length: 224 July 26, 2004 14:11 Type: N Check: 7602 ..
 Initial Score = 38 Optimized Score = 107 Significance = -0.93
 Residue Identity = 54% Matches = 134 Mismatches = 77
 Gaps = 37 Conservative Substitutions = 0

2460 2470 2480 2490 2500 2510 2520
 TACAAAGTTAGCTGGCGCAGAAGATGGTGTGATGAATGGCATCTGTGCTGCAAAATGTTGCCA--
 X TGTCTCAGATGTCCCAG 10 20
 2530 2540 2550 2560 2570 2580 2590 2590

AATAAA-TTGTCCTAGGCACGCCAA-CCCTTGT-TCCA-TACCTGATCAAAGTCAAGGCTCTGATGACAT
 ACTACAGCTGGCTGGG--GCCAACCCATGTCATTCAAGGCCTGAACTTGATGAGTTGAA-ACA-
 30 40 50 60 70 80
 2600 2610 2620 2630 2640 2650 2660
 GGTTGTTGC--CCCGAGCCAGCTGAGTCATGG-GCACATTCTGAGAAAGACTCCAAATGGGTCTCCMGG
 ANGGTGGCGTGGCTAGACA-ATATTAT-TGGATACATTGCCAA----CCACAGATG-TCCATT
 90 100 110 120 130 140
 2670 2680 2690 2700 2710 2720 2730
 GAACGGCGCTGTGAATGGTGGAAAG-CAG-TACCTTAG--CCGAGGTCACCTGGACCAGACCTCTGAAAG
 CATCATACCATCTTCTGGG-CAGCTGACTTGTACTGAG-GC-CAG--CCATTAGAT-TCGAAC
 150 160 170 180 190 200 210
 2740 X 2750 2760 2770 2780 2790
 CATCCGAGCACCPACAAGGCTATGGATTACTATGGAAAGCCAGTTCACTAA
 CATTCAGGG
 220 X

8. US-09-301-380-1 (1-4134)
 aa151738 TOIG of: aa151738 check: 8787 from: 1 to: 697
 TOIG of: aa151738 check: 8787 from: 1 to: 697
 LOCUS AA151738 697 bp mRNA linear EST 14-MAY-1997
 DEFINITION Z128n03.r1 Soares_pregnant uterus NbHPU Homo sapiens cDNA clone
 IMAGE:5_03255' similar to contains element MER22 repetitive
 element ; mRNA sequence.
 ACCESSION AA151738
 VERSION AA151738.1 GI:1720293
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Butharia; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE I (bases 1 to 697)
 AUTHORS Biller L, Lennon G, Becker M, Bonaldo M.F., Chiapelli B.,
 Chissler S., Dietrich N., DubBugre T., Favaleo A., Gish N.,
 Hultman M., Kucaba T., Lacy M., Le M., Le N.,
 Mardis E., Morris B., Morris M., Parsons J., Prange C., Riekin L.,
 Rohling T., Schellenberg K., Soares M.B., Tan F., Thierry-Mieg J.,
 Treviskis B., Underwood K., Wohldmann P., Waterston R., Wilson R.,
 and Marra M.
 TITLE Generation and analysis of 280,000 human expressed sequence tags
 JOURNAL Genome Res. 6 (9), 807-828 (1996)
 MEDLINE 9704478
 PUBMED 8889549
 COMMENT Contact: Wilson RK
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 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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 IMAGE Consortium (info@image.llnl.gov) for further information.
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 Seq Primer: -28M13 rev2 from Amersham
 High Quality sequence stop: 513.
 FEATURES Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="GDB:380873"
 /db_xref="Taxon:9606"
 /clone="IMAGE_503265"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"

